AATATTTTCCTTGACCTAATGCCATCTTGTGTCCCCTTGCAGAGCCCTATTCCTAACATGGCTGATGACTA
TGGCTCTGAATCCACATCTTCCATGGAAGACTACGTTAACTTCAACTTCACTGACTTCTACTGTGAGAAAA
ACAATGTCAGGCAGTTTGCGAGCCATTTCCTCCCACCCTTGTACTGGCTCGTGTTCATCGTGGGTGCCTTG
GGCAACAGTCTTGTTATCCTTGTCTACTGGTACTGCACAAGAGTGAAGACCATGACCGACATGTTCCTTTT
GAATTTGGCAATTGCTGACCTCCTCTTTCTTGTCACTCTTCCCTTCTGGGCCATTGCTGCTGCTGACCAGT
GGAAGTTCCAGACCTTCATGTGCAAGGTGGTCAACAGCATGTACAAGATGAACTTCTACAGCTGTGTGTTG
CTGATCATGTGCATCAGCGTGGACAGGTACATTGCCATTGCCCAGGCCATGAGAGCACATACTTGGAGGGA
GAAAAGGCTTTTGTACAGCAAAATGGTTTGCTTTACCATCTGGGTATTGGCAGCTGCTCTCTGCATCCCAG
AAATCTTATACAGCCAAATCAAGGAGGAATCCGGCATTGCTATCTGCACCATGGTTTACCCTAGCGATGAG
AGCACCAAACTGAAGTCAGCTGTCTTGACCCTGAAGGTCATTCTGGGGTTCTTCCTTCCCTTCGTGGTCAT
GGCTTGCTGCTATACCATCATCATTCACACCCTGATACAAGCCAAGAAGTCTTCCAAGCACAAAGCCCTAA
AAGTGACCATCACTGTCCTGACCGTCTTTGTCTTGTCTCAGTTTCCCTACAACTGCATTTTGTTGGTGCAG
ACCATTGACGCCTATGCCATGTTCATCTCCAACTGTGCCGTTTCCACCAACATTGACATCTGCTTCCAGGT
CACCCAGACCATCGCCTTCTTCCACAGTTGCCTGAACCCTGTTCTCTATGTTTTTGTGGGTGAGAGATTCC
GCCGGGATCTCGTGAAAACCCTGAAGAACTTGGGTTGCATCAGCCAGGCCCAGTGGGTTTCATTTACAAGG
AGAGAGGGAAGCTTGAAGCTGTCGTCTATGTTGCTGGAGACAACCTCAGGAGCACTCTCCCTCTGAGGGGT
CTTCTCTGAGGTGCATGGTTCTTTTGGAAGAAATGAGAAATACATGAAACAGTTTCCCCACTGATGGGACC
AGAGAGAGTGAAAGAGAAAGAAAACTCAGAAAGGGATGAATCTGAACTATATGATTACTTGTAGTCAGAA
TTTGCCAAAGCAAATATTTCAAAATCAACTGACTAGTGCAGGAGGCTGTTGATTGGCTCTTGACTGTGATG
CCCGCAATTCTCAAAGGAGGACTAAGGACCGGCACTGTGGAGCACCCTGGCTTTGCCACTCGCCGGAGCAT
CAATGCCGCTGCCTCTGGAGGAGCCCTTGGATTTTCTCCATGCACTGTGAACTTCTGTGGCTTCAGTTCTC
ATGCTGCCTCTTCCAAAAGGGGACACAGAAGCACTGGCTGCTGCTACAGACCGCAAAAGCAGAAAGTTTCG
TGAAAATGTCCATCTTTGGGAAATTTTCTACCCTGCTCTTGAGCCTGATAACCCATGCCAGGTCTTATAGA
TTCCTGATCTAGAACCTTTCCAGGCAATCTCAGACCTAATTTCCTTCTGTTCTCCTTGTTCTGTTCTGGGC
CAGTGAAGGTCCTTGTTCTGATTTTGAAACGATCTGCAGGTCTTGCCAGTGAACCCCTGGACAACTGACCA
CACCCACAAGGCATCCAAAGTCTGTTGGCTTCCAATCCATTTCTGTGTCCTGCTGGAGGTTTTAACCTAGA
CAAGGATTCCGCTTATTCCTTGGTATGGTGACAGTGTCTCTCCATGGCCTGAGCAGGGAGATTATAACAGC
TGGGTTCGCAGGAGCCAGCCTTGGCCCTGTTGTAGGCTTGTTCTGTTGAGTGGCACTTGCTTTGGGTCCAC
CGTCTGTCTGCTCCCTAGAAAATGGGCTGGTTCTTTTGGCCCTCTTCTTTCTGAGGCCCACTTTATTCTGA
GGAATACAGTGAGCAGATATGGGCAGCAGCCAGGTAGGGCAAAGGGGTGAAGCGCAGGCCTTGCTGGAAGG
CTATTTACTTCCATGCTTCTCCTTTTCTTACTCTATAGTGGCAACATTTTAAAAGCTTTTAACTTAGAGAT
TAGGCTGAAAAAAATAAGTAATGGAATTCACCTTTGCATCTTTTGTGTCTTTCTTATCATGATTTGGCAAA
ATGCATCACCTTTGAAAATATTTCACATATTGGAAAAGTGCTTTTTAATGTGTATATGAAGCATTAATTAC
TTGTCACTTTCTTTACCCTGTCTCAATATTTTAAGTGTGTGCAATTAAAGATCAAATAGATACATTAAGAG
TGTGAAGGCTGGTCTGAAGGTAGTGAGCTATCTCAATCGGATTGTTCACACTCAGTTACAGATTGAACTCC
TTGTTCTACTTCCCTGCTTCTCTCTACTGCAATTGACTAGTCTTTAAAAAAAAGTGTGAAGAGTAAGCAAT
AGGGATAAGGAAATAAGATCT (SEQ ID NO:1)

MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWVFIVGALGNSLVILVYWYCTRVKTMTD
MFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYSCVLLIMCISVDRYIAIAQAMRAH
TWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEESGIAICTMVYPSDESTKLKSAVLTLKVILGFFLP
FVVMACCYTIIIHTLIQAKKSSKHKALKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDI
CFQVTQTIAFFHSCLNPVLYVFVGERFRRDLVKTLKNLGCISQAQWVSFTRREGSLKLSSMLLETTSGALS
L (SEQ ID NO:2)

FIGURE 1

Underlined = deleted in targeting construct

Bold = sequence flanking Neo insert in targeting construct

AATATTTTCCTTGACCTAATGCCATCTTGTGTCCCCTTGCAGAGCCCTATTCCTAACATG
GCTGATGACTATGGCTCTGAATCCACATCTTCCATGGAAGACTACGTTAACTTCAACTTC
ACTGACTTCTACTGTGAGAAAAACAATGTCAGGCAGTTTGCGAGCCATTTCCTCCCACCC
TTGTACTGGCTCGTGTTCATCGTGGGTGCCTTGGGCAACAGTCTTGTTAT CCTTGTCTAC
TGGTACTGCACAAGAGTGAAGACCATGACCGACATGTTCCTTTTGAATTTGGCAATTGCT
GACCTCCTCTTTCTTGTCACTCTTCCCTTCTGGGCCATTGCTGCTGCTGACCAGTGGAAG
TTCCAGACCTTCATGTGCAAGGTGGTCAACAGCA **TGTACAAGATGAACTTCTACAGCTGT**
GTGTTGCTGATCATGTGCATCAGCGTGGACAGGTACATTGCCATTGCCCAGGCCATGAGA
GCACATACTTGGAGGGAGAAAAGGCTTTTGTACAGCAAAATGGTTTGCTTTACCATCTGG
GTATTGGCAGCTGCTCTCTGCATCCCAGAAATCTTATACAGCCAAATCAAGGAGGAATCC
GGCATTGCTATCTGCACCATGGTTTACCCTAGCGATGAGAGCACCAAACTGAAGTCAGCT
GTCTTGACCCTGAAGGTCATTCTGGGGTTCTTCCTTCCCTTCGTGGTCATGGCTTGCTGC
TATACCATCATCATTCACACCCTGATACAAGCCAAGAAGTCTTCCAAGCACAAAGCCCTA
AAAGTGACCATCACTGTCCTGACCGTCTTTGTCTTGTCTCAGTTTCCCTACAACTGCATT
T TGTTGGTGCAGACCATTGACGCCTATGCCATGTTCATCTCCAACTGTGCCGTTTCCACC
AACATTGACATCTGCTTCCAGGTCACCCAGACCATCGCCTTCTTCCACAGTTGCCTGAAC
CCTGTTCTCTATGTTTTTGTGGGTGAGAGATTCCGCCGGGATCTCGTGAAAACCCTGAAG
AACTTGGGTTGCATCAGCCAGGCCCAGTGGGTTTCATTTACAAGGAGAGAGGGAAGCTTG
AAGCTGTCGTCTATGTTGCTGGAGACAACCTCAGGAGCACTCTCCCTCTGAGGGGTCTTC
TCTGAGGTGCATGGTTCTTTTGGAAGAAATGAGAAATACATGAAACAGTTTCCCCACTGA
TGGGACCAGAGAGAGTGAAAGAGAAAAGAAAACTCAGAAAGGGATGAATCTGAACTATAT
GATTACTTGTAGTCAGAATTTGCCAAAGCAAATATTTCAAAATCAACTGACTAGTGCAGG
AGGCTGTTGATTGGCTCTTGACTGTGATGCCCGCAATTCTCAAAGGAGGACTAAGGACCG
GCACTGTGGAGCACCCTGGCTTTGCCACTCGCCGGAGCATCAATGCCGCTGCCTCTGGAG
GAGCCCTTGGATTTTCTCCATGCACTGTGAACTTCTGTGGCTTCAGTTCTCATGCTGCCT
CTTCCAAAAGGGGACACAGAAGCACTGGCTGCTGCTACAGACCGCAAAAGCAGAAAGTTT
CGTGAAAATGTCCATCTTTGGGAAATTTTCTACCCTGCTCTTGAGCCTGATAACCCATGC
CAGGTCTTATAGATTCCTGATCTAGAACCTTTCCAGGCAATCTCAGACCTAATTTCCTTC
TGTTCTCCTTGTTCTGTTCTGGGCCAGTGAAGGTCCTTGTTCTGATTTTGAAACGATCTG
CAGGTCTTGCCAGTGAACCCCTGGACAACTGACCACACCCACAAGGCATCCAAAGTCTGT
TGGCTTCCAATCCATTTCTGTGTCCTGCTGGAGGTTTTAACCTAGACAAGGATTCCGCTT
ATTCCTTGGTATGGTGACAGTGTCTCTCCATGGCCTGAGCAGGGAGATTATAACAGCTGG
GTTCGCAGGAGCCAGCCTTGGCCCTGTTGTAGGCTTGTTCTGTTGAGTGGCACTTGCTTT
GGGTCCACCGTCTGTCTGCTCCCTAGAAAATGGGCTGGTTCTTTTGGCCCTCTTCTTTCT
GAGGCCCACTTTATTCTGAGGAATACAGTGAGCAGATATGGGCAGCAGCCAGGTAGGGCA
AAGGGGTGAAGCGCAGGCCTTGCTGGAAGGCTATTTACTTCCATGCTTCTCCTTTTCTTA
CTCTATAGTGGCAACATTTTAAAAGCTTTTAACTTAGAGATTAGGCTGAAAAAAATAAGT
AATGGAATTCACCTTTGCATCTTTTGTGTCTTTCTTATCATGATTTGGCAAAATGCATCA
CCTTTGAAAATATTTCACATATTGGAAAAGTGCTTTTTAATGTGTATATGAAGCATTAAT
TACTTGTCACTTTCTTTACCCTGTCTCAATATTTTAAGTGTGTGCAATTAAAGATCAAAT
AGATACATTAAGAGTGTGAAGGCTGGTCTGAAGGTAGTGAGCTATCTCAATCGGATTGTT
CACACTCAGTTACAGATTGAACTCCTTGTTCTACTTCCCTGCTTCTCTCTACTGCAATTG
ACTAGTCTTTAAAAAAAAGTGTGAAGAGTAAGCAATAGGGATAAGGAAATAAGATCT

FIGURE 2A

Gene Sequence Structure *
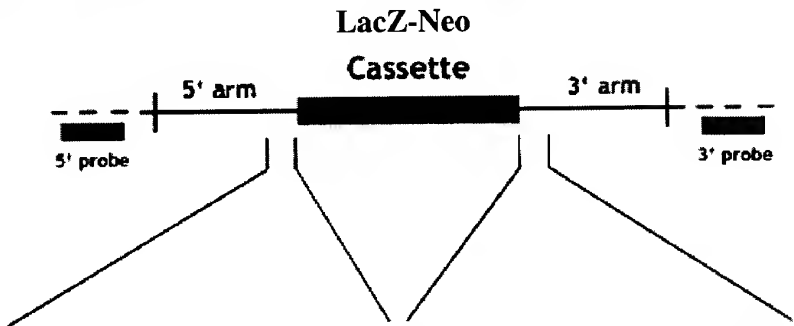
231 bp   Sequence Deleted   394 bp

Size of CDS: 2577 bp

Targeting Vector* (genomic sequence)

Construct Number: 3340

LacZ-Neo Cassette

5' arm

Cassette

3' arm

5' probe

3' probe

Arm Length:
5': 2.7 kb
3': 4 kb

——————— Targeting Vector
– – – – – Endogenous Locus

* Not drawn to scale

```
5'>TATTCCTTACAGAGCCTTATT
CCTGGCATGTTTGATGACTTCAGC
TATGACTCCACTGCTTCCACAGAT
GACTACATGAATTTGAATTTCAGT
AGCTTCTTCTGTAAGAAAAATAAT
GTCAGGCAGTTTGCAAGCCATTTT
CTCCCACCTCTGTACTGGCTTGTG
TTCATTGTGGGCACCTTGGGCAAC
AGCCTGGTCAT<3'
(SEQ.ID.NO.3)
```

```
5'>TGTACAAGATGAACTTCTACA
GCTGTGTGCTTCTCATCATGTGCA
TCAGTGTGGACAGATACATTGCCA
TTGTACAGGCCATGAAGGCTCAGG
TCTGGAGGCAGAAAAGGCCGCTAT
ACAGCAAGATGGTCTGCATTACCA
TCTGGGTGATGGCAGCTGTGCTCT
GCACCCCAGAAATCCTGTACAGTC
AAGTCAGTGGG<3'
(SEQ.ID.NO.4)
```

FIGURE 2B